WEST Search History

DATE: Thursday, February 13, 2003

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,DWPI; PLUR=YES; OP=ADJ			
L1	erikson-G$.in. or Daksis-J$.in.	12	L1
L2	5030557	98	L2
L3	enhanc$ near10 hybridiz$	1179	L3
L4	hairpin near5 block$ agent	0	L4
L5	hairpin near block$	9	L5
L6	hairpin same block$	372	L6
L7	probe same target same hybridiz$	6923	L7
L8	L7 and l3	687	L8
L9	L8 and l1	1	L9
L10	L8 and l6	16	L10
L11	6265170.pn. or 5770365.pn.	4	L11

END OF SEARCH HISTORY

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 NEWS  3  Apr 09  BEILSTEIN: Reload and Implementation of a New Subject Area
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 NEWS  5  Apr 19  US Patent Applications available in IFICDB, IFIPAT, and
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 NEWS  6  Apr 22  Records from IP.com available in CAPLUS, HCAPLUS, and
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 NEWS  7  Apr 22  BIOSIS Gene Names now available in TOXCENTER
 NEWS  8  Apr 22  Federal Research in Progress (FEDRIP) now available
 NEWS  9  Jun 03  New e-mail delivery for search results now available
 NEWS 10  Jun 10  MEDLINE Reload
 NEWS 11  Jun 10  PCTFULL has been reloaded
 NEWS 12  Jul 02  FOREGE no longer contains STANDARDS file segment
 NEWS 13  Jul 22  USAN to be reloaded July 28, 2002;
                  saved answer sets no longer valid
 NEWS 14  Jul 29  Enhanced polymer searching in REGISTRY
 NEWS 15  Jul 30  NETFIRST to be removed from STN
 NEWS 16  Aug 08  CANCERLIT reload
 NEWS 17  Aug 08  PHARMAMarketLetter(PHARMAML) - new on STN
 NEWS 18  Aug 08  NTIS has been reloaded and enhanced
 NEWS 19  Aug 19  Aquatic Toxicity Information Retrieval (AQUIRE)
                  now available on STN
 NEWS 20  Aug 19  IFIPAT, IFICDB, and IFIUDB have been reloaded
 NEWS 21  Aug 19  The MEDLINE file segment of TOXCENTER has been reloaded
 NEWS 22  Aug 26  Sequence searching in REGISTRY enhanced
 NEWS 23  Sep 03  JAPIO has been reloaded and enhanced
 NEWS 24  Sep 16  Experimental properties added to the REGISTRY file
 NEWS 25  Sep 16  CA Section Thesaurus available in CAPLUS and CA
 NEWS 26  Oct 01  CASREACT Enriched with Reactions from 1907 to 1985
 NEWS 27  Oct 21  EVENTLINE has been reloaded
 NEWS 28  Oct 24  BEILSTEIN adds new search fields
 NEWS 29  Oct 24  Nutraceuticals International (NUTRACEUT) now available on
STN
 NEWS 30  Oct 25  MEDLINE SDI run of October 8, 2002
 NEWS 31  Nov 18  DKILIT has been renamed APOLLIT
 NEWS 32  Nov 25  More calculated properties added to REGISTRY
 NEWS 33  Dec 02  TIBKAT will be removed from STN
 NEWS 34  Dec 04  CSA files on STN
 NEWS 35  Dec 17  PCTFULL now covers WP/PCT Applications from 1978 to date
 NEWS 36  Dec 17  TOXCENTER enhanced with additional content
 NEWS 37  Dec 17  Adis Clinical Trials Insight now available on STN
 NEWS 38  Dec 30  ISMEC no longer available
 NEWS 39  Jan 13  Indexing added to some pre-1967 records in CA/CAPLUS
 NEWS 40  Jan 21  NUTRACEUT offering one free connect hour in February 2003
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NEWS 41  Jan 21  PHARMAML offering one free connect hour in February 2003
NEWS 42  Jan 29  Simultaneous left and right truncation added to COMPENDEX,
                 ENERGY, INSPEC

NEWS EXPRESS  January 6 CURRENT WINDOWS VERSION IS V6.01a,
              CURRENT MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
              AND CURRENT DISCOVER FILE IS DATED 01 OCTOBER 2002
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7 FILES IN THE FILE LIST

=> search Erikson G?/au or Daksis J?/au
L1          134 ERIKSON G?/AU OR DAKSIS J?/AU

=> s enhanc? and hybridiz
=> s enhanc (P) hybridiz?
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'ENHANC (P) HYBRIDIZ?'
L2            0 ENHANC (P) HYBRIDIZ?

=> s enhanc? and hybridiz?
L3        29614 ENHANC? AND HYBRIDIZ?

=> s hairpin (s) block###
L4          752 HAIRPIN (S) BLOCK###

=> s helper (s) oligonucl?
L5          697 HELPER (S) OLIGONUCL?

=> s probe (s) target(s) hybridiz?
L6         6618 PROBE (S) TARGET(S) HYBRIDIZ?
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     FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS'
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L1           134 SEARCH ERIKSON G?/AU OR DAKSIS J?/AU
L2             0 S ENHANC (P) HYBRIDIZ?
L3         29614 S ENHANC? AND HYBRIDIZ?
L4           752 S HAIRPIN (S) BLOCK###
L5           697 S HELPER (S) OLIGONUCL?
L6          6618 S PROBE (S) TARGET(S) HYBRIDIZ?

=> s l1 and l3
L7             4 L1 AND L3

=> s l3 and l6
L8           462 L3 AND L6

=> s l8 and (l4 or l5)
L9            10 L8 AND (L4 OR L5)

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     FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS'
     ENTERED AT 13:13:57 ON 13 FEB 2003
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L6          6618 S PROBE (S) TARGET(S) HYBRIDIZ?
L7             4 S L1 AND L3
L8           462 S L3 AND L6
L9            10 S L8 AND (L4 OR L5)

=> d ibib abs l7 1-4

L7   ANSWER 1 OF 4  BIOSIS  COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER:   2001:440564  BIOSIS
DOCUMENT NUMBER:    PREV200100440564
TITLE:              Homogenous assay of duplex of triplex hybridization
                    by means of multiple measurements under varied
conditions.
AUTHOR(S):          Picard, Pierre (1); Daksis, Jasmine I.;
                    Erikson, Glen H.
CORPORATE SOURCE:   (1) Brampton Canada
                    ASSIGNEE: Ingeneus Corporation, Bridgetown, Barbados
PATENT INFORMATION: US 6265170 July 24, 2001
SOURCE:             Official Gazette of the United States Patent and Trademark
                    Office Patents, (July 24, 2001) Vol. 1248, No. 4, pp. No
                    Pagination. e-file.
                    ISSN: 0098-1133.
DOCUMENT TYPE:      Patent
LANGUAGE:           English
AB   The invention provides homogeneous assay methods for nucleic acid
     hybridization, detection and evaluation. The assay includes
     obtaining signals from a test sample both before and during the
     application of a voltage to the test sample and correlating the signals,
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each of which is indicative of the binding affinity of the probe and the target to each other. The assay enables determining an extent of matching between the probe and the target, as the voltage can be calibrated so as to destabilize significantly any **hybridization** except perfectly complementary **hybridization**. The signals whose magnitude is correlated with binding affinity can be electrical conductance and/or fluorescent intensity. Preferably, both signal pairs are measured and compared so as to **enhance** the reliability of the assay. The assay can detect specific **hybridization** between single-stranded probes and non-denatured double-stranded targets to form triplexes, thus obviating the need to denature the targets. The assay methods can also be applied to duplex **hybridization** complexes.

L7 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:736774 CAPLUS
DOCUMENT NUMBER: 137:258475
TITLE: Homogeneous assay of nucleic acid **hybridization** by means of multiple measurements under varied conditions
INVENTOR(S): **Erikson, Glen H.; Daksis, Jasmine I.** ; Picard, Pierre
PATENT ASSIGNEE(S): Turks/Caicos I.
SOURCE: U.S. Pat. Appl. Publ., 22 pp., Cont.-in-part of U.S. 6,265,170.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002137056	A1	20020926	US 2001-911047	20010723
US 6265170	B1	20010724	US 2000-490273	20000124
US 2002123066	A1	20020905	US 2002-120092	20020410
WO 2003010506	A2	20030206	WO 2002-IB2788	20020715

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2000-490273 A2 20000124
US 2001-911047 A2 20010723

AB A method for homogeneously assaying biopolymer bonding, specifically nucleic acid **hybridization**, includes obtaining signals from a test sample before, during and/or after the application of stimulus to the test sample and correlating the signals. The signals, whose magnitude correlate with binding affinity, can be, for example, elec. conductance and/or fluorescent intensity. The stimulus can be, for example, elec. voltage and/or laser radiation. Preferably, different types of signals are measured and compared so as to **enhance** the reliability of the assay.

L7 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:696538 CAPLUS
DOCUMENT NUMBER: 137:227601
TITLE: Nucleic acid binding **enhancement** by conjugation with nucleotides, nucleosides, bases and/or their analogs for improved degree and specificity of **hybridization**
INVENTOR(S): **Erikson, Glen H.; Daksis, Jasmine I.**
PATENT ASSIGNEE(S): Ingeneus Corporation, Barbados
SOURCE: U.S. Pat. Appl. Publ., 9 pp., Cont.-in-part of U. S. Ser. No. 909,496.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 7
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002127590	A1	20020912	US 2002-80767	20020222
US 6403313	B1	20020611	US 1999-468679	19991221
US 6420115	B1	20020716	US 2000-613263	20000710
US 2002031775	A1	20020314	US 2001-909496	20010720
WO 2002024946	A2	20020328	WO 2001-IB1643	20010910
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2001084350	A5	20020402	AU 2001-84350	20010910

PRIORITY APPLN. INFO.:

US 1999-468679	A2	19991221
US 2000-613263	A2	20000710
US 2000-664827	A2	20000919
US 2001-281547P	P	20010404
US 2001-909496	A2	20010720
WO 2001-IB1643	W	20010910

AB An improved method of forming a specific complex between a probe contg. probe nucleobases and a target contg. target nucleobases, includes mixing the probe and the target under **hybridizing** conditions, wherein the probe and/or the target is conjugated to a blocking agent, which **enhances** the avidity and/or specificity of **hybridization** , whether by Watson-Crick motif or by homologous binding motif. The blocking agent contains at least one nucleobase and can be, e.g., a free nucleobase, a nucleoside or a nucleotide. Conjugation **enhances** **hybridization** by hindering the probe and/or target from existing in a conformation antithetical to **hybridization**. Thus, reaction of 2 pmoles of a 15-mer single-stranded DNA probe contg. 6 adenine bases (conjugated with 3 pmoles of thymine) with 2 pmoles of a wild-type antisense strand (50-mer) in the presence of YOYO-1 results in 78% increased formation of parallel homologous complexes between perfectly homologous sequences. By contrast, the efficiency of formation of parallel homologous complexes contg. a 1-bp A-G mismatch was increased by only 16% when the probe was conjugated 25% with thymine.

L7 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:537425 CAPLUS
DOCUMENT NUMBER: 135:133083
TITLE: Homogenous assay of duplex of triplex

hybridization by means of multiple measurements under varied conditions

INVENTOR(S): Picard, Pierre; **Daksis, Jasmine I.**; **Erikson, Glen H.**

PATENT ASSIGNEE(S): Ingeneus Corporation, Barbados

SOURCE: U.S., 22 pp.
CODEN: USXXAM

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6265170	B1	20010724	US 2000-490273	20000124
WO 2001053526	A2	20010726	WO 2001-IB77	20010123
WO 2001053526	A3	20020613		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1250459	A2	20021023	EP 2001-902567	20010123
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
US 2002137056	A1	20020926	US 2001-911047	20010723
US 2002123066	A1	20020905	US 2002-120092	20020410

PRIORITY APPLN. INFO.:

US 2000-490273	A	20000124
WO 2001-IB77	W	20010123
US 2001-911047	A2	20010723

AB The invention provides homogeneous assay methods for nucleic acid **hybridization**, detection and evaluation. The assay includes obtaining signals from a test sample both before and during the application of a voltage to the test sample and correlating the signals, each of which is indicative of the binding affinity of the probe and the target to each other. The assay enables detg. an extent of matching between the probe and the target, as the voltage can be calibrated so as to destabilize significantly any **hybridization** except perfectly complementary **hybridization**. The signals whose magnitude is correlated with binding affinity can be elec. conductance and/or fluorescent intensity. Preferably, both signal pairs are measured and compared so as to **enhance** the reliability of the assay. The assay can detect specific **hybridization** between single-stranded probes and non-denatured double-stranded targets to form triplexes, thus obviating the need to denature the targets. The assay methods can also be applied to duplex **hybridization** complexes. The invention can discriminate between perfectly matched dsDNA:PNA triplex hybrids and those contg. 1 bp or 2 bp mismatches. Intercalation by YOYO-1 facilitated the formation of the dsDNA-PNA triplexes and dsDNA-ssDNA triplexes.

REFERENCE COUNT: 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS'
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L1          134 SEARCH ERIKSON G?/AU OR DAKSIS J?/AU
L2            0 S ENHANC (P) HYBRIDIZ?
L3        29614 S ENHANC? AND HYBRIDIZ?
L4          752 S HAIRPIN (S) BLOCK###
L5          697 S HELPER (S) OLIGONUCL?
L6         6618 S PROBE (S) TARGET(S) HYBRIDIZ?
L7            4 S L1 AND L3
L8          462 S L3 AND L6
L9           10 S L8 AND (L4 OR L5)
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=> d ibib abs l9 1-10

L9 ANSWER 1 OF 10 MEDLINE

ACCESSION NUMBER: 2001075808 MEDLINE
DOCUMENT NUMBER: 20378673 PubMed ID: 10919826
TITLE: Unlabeled **helper oligonucleotides** increase the in situ accessibility to 16S rRNA of fluorescently labeled **oligonucleotide** probes.
AUTHOR: Fuchs B M; Glockner F O; Wulf J; Amann R
CORPORATE SOURCE: Max-Planck-Institut fur Marine Mikrobiologie, D-28359 Bremen, Germany.. bfuchs@mpi-bremen.de
SOURCE: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (2000 Aug) 66 (8) 3603-7.
Journal code: 7605801. ISSN: 0099-2240.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010104

AB **Target** site inaccessibility represents a significant problem for fluorescence in situ **hybridization** (FISH) of 16S rRNA with **oligonucleotide** probes. Here, unlabeled **oligonucleotides** (helpers) that bind adjacent to the **probe target** site were evaluated for their potential to increase weak **probe hybridization** signals in Escherichia coli DSM 30083(T). The use of helpers **enhanced** the fluorescence signal of all six probes examined at least fourfold. In one case, the signal of **probe** Eco474 was increased 25-fold with the use of a single **helper probe**, H440-2. In another case, four unlabeled helpers raised the FISH signal of a formerly weak **probe**, Eco585, to the level of the brightest monolabeled **oligonucleotide** probes available for E. coli. The temperature of dissociation and the mismatch discrimination of probes were not significantly influenced by the addition of helpers. Therefore, using helpers should not cause labeling of additional nontarget organisms at a defined stringency of **hybridization**. However, the **helper** action is based on sequence-specific binding, and there is thus a potential for narrowing the **target** group which must be considered when designing helpers. We conclude that helpers can open inaccessible rRNA regions for FISH with **oligonucleotide** probes and will thereby further improve the applicability of this technique for in situ identification of microorganisms.

a probe to the 430-500 region of Salmonella 16 S rRNA, as well as **helper oligonucleotides** I and/or II. In an overnight **hybridization** protocol using probe alone, probe/I, probe/II, or probe/I/II, percent hybrid found was 1.8, 68.5, 68.0, or 83.1%, resp. The Tm of the probe alone, probe/I, and probe/II were 59.degree., 63.5.degree., and 63.0.degree., resp. A kit contg. **helper oligonucleotides** is claimed.

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=> d his

     (FILE 'HOME' ENTERED AT 13:09:57 ON 13 FEB 2003)

     FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS'
     ENTERED AT 13:13:57 ON 13 FEB 2003
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L2             0 S ENHANC (P) HYBRIDIZ?
L3         29614 S ENHANC? AND HYBRIDIZ?
L4           752 S HAIRPIN (S) BLOCK###
L5           697 S HELPER (S) OLIGONUCL?
L6          6618 S PROBE (S) TARGET(S) HYBRIDIZ?
L7             4 S L1 AND L3
L8           462 S L3 AND L6
L9            10 S L8 AND (L4 OR L5)

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ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF
LOGOFF? (Y)/N/HOLD:y
COST IN U.S. DOLLARS                                  SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                      74.64      76.11

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)            SINCE FILE      TOTAL
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CA SUBSCRIBER PRICE                                      -4.56      -4.56

STN INTERNATIONAL LOGOFF AT 13:28:35 ON 13 FEB 2003
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L9 ANSWER 2 OF 10 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 2002-16605 BIOTECHDS
TITLE: Novel **oligonucleotides** functioning as **hybridization** probes, **helper** probes and/or primers, targeted to nucleic acid sequences derived from Cryptosporidium organisms, useful for detecting the organism in a test sample;
involving DNA probe, DNA primer and **hybridization** for use in protozoon detection in water, excrement and food samples
AUTHOR: CUNNINGHAM M M; STULL P D; WEISBURG W G
PATENT ASSIGNEE: GEN-PROBE INC
PATENT INFO: WO 2002022890 21 Mar 2002
APPLICATION INFO: WO 2000-US42192 12 Sep 2000
PRIORITY INFO: US 2000-232028 12 Sep 2000
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2002-454395 [48]
AN 2002-16605 BIOTECHDS
AB DERWENT ABSTRACT:
NOVELTY - **Oligonucleotides** functioning as **hybridization** assay probes, **helper** probes and/or amplification primers, targeted to nucleic acid sequences derived from Cryptosporidium (Cp) organisms, are new.
DETAILED DESCRIPTION - The **oligonucleotide** may be: (a) **hybridization** assay **probe** (I) comprising an **oligonucleotide** which **hybridizes** to a **target** sequence present in nucleic acid derived from Cp organism or C.parvum in a test sample under stringent conditions to form (I):**target** hybrid stable for detection, where (I) has an at least 10 contiguous base region that is 80% complementary to an at least 10 contiguous base region present in the **target** sequence e.g. (S1-S4) (all of which are derived from a Cp organism) or (S5-S20) (all of which are derived from C.parvum), where the **probe** complementary to sequence of (S1)-(S4) does not **hybridize** to nucleic acid derived from non-Cp organism, and the **probe** complementary to sequence of (S5)-(S20) does not **hybridize** to a nucleic acid derived from C.muris, C.baileyi, C.wrairi, in the test sample, to form **probe** :non-**target** hybrid stable for detection under stringent conditions; (b) a **probe** mix (II) comprising (I) and one or more **helper oligonucleotides** with an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a **target** sequence e.g. (S21-S44), where (S21-29) are derived from a Cp organism and (S30-44) are derived from a C.parvum organism; or (c) an amplification primer (III) for use in amplifying a nucleic acid sequence present in nucleic acid derived from Cp organism under amplification conditions, where the primer comprises an **oligonucleotide** with at least 10 contiguous base region that is at least 80% complementary to at least 10 contiguous base region present in a **target** sequence e.g. (S45-S68) (the amplification primer is directed to 18S ribosomal nucleic acid derived from Cp or C.parvum organism). INDEPENDENT CLAIMS are also included for: (1) a set of amplification primers (IV) for use in amplifying a nucleic acid sequences present in nucleic acid derived from Cp organisms under amplification conditions, where at least two primers of the set of primers comprises an **oligonucleotide** with at least 10

contiguous base region that is at least 80% complementary to an at least 10 contiguous base region present in **target** sequence of (S45)-(S68), where the primers of the set of primers optionally include a 5' sequence that is recognized by an RNA polymerase or **enhances** initiation or elongation by a RNA polymerase; (2) an **oligonucleotide** (V) for use in determining the presence of a C.parvum organism in a test sample, the **oligonucleotide** with at least 10 contiguous base region that is at least 80% complementary to an at least 10 contiguous base region present in **target** sequence of (S1)-(S20), (S45)-(S67) or (S68), where the **oligonucleotide** optionally includes a 5' sequence which is recognized by an RNA polymerase or which **enhances** initiation or elongation by RNA polymerase; (3) a kit (VI) comprising, in packaged combination two or more (V); (4) a kit (VII) comprising in packaged combination (I) and at least one **helper oligonucleotide** with at least 10 contiguous base region that is at least 80% complementary to an at least 10 contiguous base region present in **target** sequence of (S21)-(S44); (5) a kit (VIII) comprising in packaged combination, (I) and (III); (6) a kit (IX) comprising in packaged combination, two or more amplification primers, where at least two of the primers are selected from (IV); and (7) obtaining (M1) purified RNA from a viable oocyst comprises (a) centrifuging a fluid sample suspected of containing oocysts at a speed and for a period of time sufficient to concentrate the oocysts within a vessel containing the fluid sample; (b) removing a supernatant from the vessel; (c) resuspending the concentrated oocysts, if present, in a buffered solution; (d) agitating the buffered solution in the presence of several particles at a rate and for a period of time sufficient to lyse the oocysts and release RNA from them; (e) immobilizing the released RNA on a RNA-binding filter; (f) purifying the released RNA by washing the filter one or more times with a buffered solution to remove oocyst components other than the released RNA; and (g) removing the purified RNA from the filter. CTATCAGCTTTAGACGGTAGGG (S1) CUAUCAGCUUUAGACGGUAGGG (S2) CCCTACCGTCTAAAGCTGATAG (S3) CCCUACCGUCUAAAGCUGAUAG (S4) GCGAAAAAACTCGACTTTATGGAAGGG (S5) GTTAAAGACAAACTAATGCGAAAGC (S8) GUUAAAGACAAACUAAUGCGAAAGC (S12) CAACCCTTCCATAAAGTCGAGTTTT (S15) GCUUUCGCAUUAGUUUGUCUUUAAC (S20) GACATATCATTCAAGTTTCTGAC (S21) GUCAGAAACUUGAAUGAUAUGUC (S27) GGAUAACCGUGGUAAUUCUAGAGCUAAUACAU (S32) UAUAUUGGUUCUUUAUCUAAUAAAUACAA (S44) GCCATGCATGTCTAAGTATAAAC (S45) GCCAAGGATGTTTTCATTAATC (S50) GUAUUUAACAGUCAGAGGUG (S55) CTGCCTTCCTTAGATGTGGTAG (S60) CCGUAAAGUUAUUAUGAGUCACC (S65) GAUUAAUGAAAACAUCCUUGGC (S68)

WIDER DISCLOSURE - The following are disclosed: (1) compositions comprising a nucleic acid hybrid found between (I) and **target** nucleic acid under stringent **hybridization** assay conditions; (2) compositions comprising nucleic acid hybrids formed between the **helper probe** and **target** nucleic acid under stringent **hybridization** assay conditions; (3) a nucleic acid hybrid formed between an amplification primer and **target** nucleic acid under amplification conditions; (4) compositions for determining the presence or amount of a Cp organism in test sample

comprising nucleic acid hybrid derived from Cp organism and a **hybridization** assay **probe** comprising **oligonucleotide** with or substantially corresponding to base sequence of (S1)-(S4); (5) compositions for determining presence of an amount of C.parvum organism present in test sample comprising nucleic acid hybrid formed between **target** nucleic acid derived from C.parvum organism and **hybridization** assay **probe** which comprises an **oligonucleotide** with or substantially corresponding to sequence of (S5)-(S20); and (6) compositions for amplifying **target** sequences present in **target** nucleic acid derived from Cp, where the compositions comprise nucleic acid hybrid formed between a **target** nucleic acid and amplification primer comprising an **oligonucleotide** with or substantially corresponding to base sequence of (S45)-(S67) or (S68).

BIOTECHNOLOGY - Preferred **Oligonucleotide**: (I) or (III) comprises an **oligonucleotide** with at least 10 contiguous base region that is at least 90% (preferably 100%) complementary to an at least 10 contiguous base region present is the **target** sequence. Preferably, the base sequence of the **oligonucleotide** is 80% complementary to the base sequence of the **target** sequence, and thus the base sequence of the **probe** or primer is at least 80% complementary to the base sequence of the **target** sequence. Optionally, the base sequence of the **probe** or primer is fully complementary to the base sequence of the **target** sequence. (I) is up to 100 bases in length, preferably 12-50 (more preferably, 18-35) bases in length. The **probe** contains base sequences that **hybridize** to each other when not **hybridized** to the **target** sequence under the stringent conditions. Optionally, the **probe** comprises one or more base sequences which do not stably **hybridize** to nucleic acid derived from Cp organisms, or to nucleic acid derived from a non-**target** organism present in the test sample under stringent conditions, where the **probe** **hybridizes** to two of the one or more base sequences, where the two base sequences **hybridize** to each other when the **probe** is not **hybridized** to the **target** sequence under the stringent conditions. (I) further comprises a detectable label of a group of interacting labels including a luminescent or a quencher label. The **oligonucleotides** include at least one ribonucleotide modified to include 2'-O-methyl substitution to the ribofuranosyl moiety, and a pseudo peptide backbone joins at least a portion of the bases of the **oligonucleotide**. (III) is 18-40 bases in length and optionally includes the 5' sequence which is recognized by an RNA polymerase or which **enhances** initiation or elongation by an RNA polymerase. Preferably, the primer includes a 5' sequence described above. The 5' sequence which is recognized by RNA polymerase or which **enhances** initiation or elongation by RNA polymerase is a T7 promoter (P1). The primer optionally contains base sequences which **hybridize** to each other when not **hybridized** to the **target** sequence under the amplification conditions. The primer further includes a group of interacting labels as described above. (IV) includes first and second primers whose **target** sequences are any one of (S45)-(S68). The base sequence of (V) is at least 80% complementary (fully complementary) to the base sequence of the **target** sequence.

AATTTAATACGACTCACTATAGGGAGA (P1) Preferred Kit: (VI) comprises two **oligonucleotides**, where the first **oligonucleotide** is complementary to a **target** sequence of any one of (S1)-(S20) and a second **oligonucleotide** complementary to a **target** sequence of (S45)-(S67) or (S68). (VIII) further comprises at least one

helper oligonucleotide with at least 10 contiguous base region which is at least 80% complementary to 10 contiguous base region in a **target** sequence of (S21)-(S43) or (S44). Preferred Method: In (M1), the agitating step includes oscillating the vessel containing the buffered solution. The particles have a spherical shape and an average diameter in the range of about 0.1-2.5 mm.

USE - (I) (complementary to a **target** sequence of (S1)-(S4)) is useful for determining the presence of Cp organism in a test sample, where the formation of (I):**target** hybrid is determined, and (I) complementary to **target** sequence of (S5)-(S20) is useful determining presence of C.parvum in a sample. For detecting C.parvum, the method further involves providing (III). (II) or (IV) is useful for amplifying Cp nucleic acid which may be present in a test sample. The method further involves determining the presence of amplified **target** sequence in test sample with a **hybridization** assay **probe** (claimed). (I) is useful for determining the presence of Cp organisms in general, and C.parvum organisms in particular in test samples of water, feces, food or other sample media.

ADVANTAGE - The **hybridization** assay probes are able to distinguish Cp and also C.parvum nucleic acids from non-Cp nucleic acids because of the ability of the **probe** to differentially **hybridize** to Cp nucleic acids under stringent **hybridization** assay conditions.

EXAMPLE - Amplification of a **target** sequence of Cryptosporidium rRNA and detection of the amplified rRNA using a **hybridization** assay **probe** specific for Cryptosporidium-derived nucleic acid was carried out as follows. Cryptosporidium **hybridization** assay **probe** with the base sequence of (A) was synthesized to include a non-nucleotide linker positioned between nucleotides 11 and 12. This **hybridization** assay **probe** was of the same sense as the Cryptosporidium **target** rRNA and was used to detect the product of a transcription-mediated amplification described by Kacian et al., in U.S. Patent Nos. 5,399,491 and 5,480,784. Ribosomal RNA from C.parvum and C.muris was separately amplified using a promoter-primer with a 5' end promoter base sequence of (S1), a 3' end sense template-specific base sequence of (S2),a primer with an antisense template-specific base sequence of (B), a promoter-primer with a 5' end promoter base sequence of (S1), a 3' end sense template-specific base sequence of (S2), and a primer with an antisense template-specific base sequence of (C). The samples were incubated after amplification. Following a 60 minute incubation at 42 degrees Centigrade in the circulating water bath, 100 microl 1X **Hybridization** Reagent containing 100 fmol of the **hybridization** assay **probe** was added to each tube, the samples were incubated for 30 minutes at 60 degrees Centigrade in the circulating water bath, and the signal from the annealed **hybridization** assay probes was detected. Sample sets with an average relative light units (RLU) value greater than 10-fold the average RLU value for the negative control indicated amplification of the **target** rRNA, and sample sets with an average RLU value less than 10-fold the average RLU for the negative control indicated no amplification of the **target** rRNA. CTATCAGCTTTAGACGGTAGGG (A) AATTTAATACGACTCACTATAGGGAGA (S1) CTGCCTTCCTTAGATGTGGTAG (S2) GCCATGCATGTCTAAGTATAAAC (B) GGATAACCGTGGTAATTCTAGAG (C) (133 pages)

L9 ANSWER 3 OF 10 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 1989-10053 BIOTECHDS
TITLE: **Enhancing** nucleic acid **hybridization**;

using a **helper** DNA **oligonucleotide** which **hybridizes** with the **target** in a different region than the DNA **probe**

PATENT ASSIGNEE: M.L.Technol.Ventures
PATENT INFO: EP 318245 31 May 1989
APPLICATION INFO: EP 1988-311036 22 Nov 1988
PRIORITY INFO: US 1987-124975 24 Nov 1987
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 1989-159301 [22]
AN 1989-10053 BIOTECHDS
AB A new process for **enhancing** binding between a nucleotide **probe** and a complementary nucleotide sequence in single-stranded **target** nucleic acid involves adding a **helper oligonucleotide**, which **hybridizes** with the **target** nucleic acid in a different region than the **probe** , to the **target**. The **target** nucleic acid is DNA, mRNA, rRNA, tRNA or other small nucleic acid. The **probe** (10-50 nucleotides) and the **helper oligonucleotide** (10-100 nucleotides) may be DNA with a diphosphate ester, alkyl, arylphosphate, or phosphorothioate backbone. The **probe** may be labeled with 125I or an acridium ester. A new duplex nucleic acid comprises a hybrid of a nucleotide **probe** and a **target** nucleic acid to which a **helper oligonucleotide** is **hybridized** . The **helper oligonucleotide** imposes a secondary and tertiary structure on the targeted region, accelerating the rate of **probe** binding. The **helper oligonucleotide** can also raise melting temp. of the hybrid of a relatively short **probe** and its intended **target**, so that assays for organisms which occur in environments populated by closely related organisms can be obtained with improved specificity. (17pp)

L9 ANSWER 4 OF 10 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 2000285313 EMBASE
TITLE: Unlabeled **helper oligonucleotides** increase the in situ accessibility to 16S rRNA of fluorescently labeled **oligonucleotide** probes.
AUTHOR: Fuchs B.M.; Glockner F.O.; Wulf J.; Amann R.
CORPORATE SOURCE: B.M. Fuchs, Max-Planck-Inst. fur Mar. Mikrobiol., Celsiusstr. 1, D-28359 Bremen, Germany. bfuchs@mpi-bremen.de
SOURCE: Applied and Environmental Microbiology, (2000) 66/8 (3603-3607).
Refs: 17
ISSN: 0099-2240 CODEN: AEMIDF
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English
AB **Target** site inaccessibility represents a significant problem for fluorescence in situ **hybridization** (FISH) of 16S rRNA with **oligonucleotide** probes. Here, unlabeled **oligonucleotides** (helpers) that bind adjacent to the **probe target** site were evaluated for their potential to increase weak **probe hybridization** signals in Escherichia coli DSM 30083(T). The use of helpers **enhanced** the fluorescence signal of all six probes examined at least fourfold. In one case, the signal of **probe** Eco474 was increased 25-fold with the use of a single **helper probe**, H440-2. In another case, four unlabeled helpers raised the FISH signal of a formerly weak **probe**, Eco585, to the level of

the brightest monolabeled **oligonucleotide** probes available for E. coli. The temperature of dissociation and the mismatch discrimination of probes were not significantly influenced by the addition of helpers. Therefore, using helpers should not cause labeling of additional nontarget organisms at a defined stringency of **hybridization**. However, the **helper** action is based on sequence-specific binding, and there is thus a potential for narrowing the **target** group which must be considered when designing helpers. We conclude that helpers can open inaccessible rRNA regions for FISH with **oligonucleotide** probes and will thereby further improve the applicability of this technique for in situ identification of microorganisms.

L9 ANSWER 5 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2000:424485 BIOSIS
DOCUMENT NUMBER: PREV200000424485
TITLE: Unlabeled **helper oligonucleotides** increase the in situ accessibility to 16S rRNA of fluorescently labeled **oligonucleotide** probes.
AUTHOR(S): Fuchs, Bernhard M. (1); Gloeckner, Frank Oliver; Wulf, Joerg; Amann, Rudolf
CORPORATE SOURCE: (1) Max-Planck-Institut fuer Marine Mikrobiologie, Celsiusstr. 1, D-28359, Bremen Germany
SOURCE: Applied and Environmental Microbiology, (August, 2000) Vol. 66, No. 8, pp. 3603-3607. print.
ISSN: 0099-2240.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB **Target** site inaccessibility represents a significant problem for fluorescence in situ **hybridization** (FISH) of 16S rRNA with **oligonucleotide** probes. Here, unlabeled **oligonucleotides** (helpers) that bind adjacent to the **probe target** site were evaluated for their potential to increase weak **probe hybridization** signals in Escherichia coli DSM 30083T. The use of helpers **enhanced** the fluorescence signal of all six probes examined at least fourfold. In one case, the signal of **probe** Eco474 was increased 25-fold with the use of a single **helper probe**, H440-2. In another case, four unlabeled helpers raised the FISH signal of a formerly weak **probe**, Eco585, to the level of the brightest monolabeled **oligonucleotide** probes available for E. coli. The temperature of dissociation and the mismatch discrimination of probes were not significantly influenced by the addition of helpers. Therefore, using helpers should not cause labeling of additional nontarget organisms at a defined stringency of **hybridization**. However, the **helper** action is based on sequence-specific binding, and there is thus a potential for narrowing the **target** group which must be considered when designing helpers. We conclude that helpers can open inaccessible rRNA regions for FISH with **oligonucleotide** probes and will thereby further improve the applicability of this technique for in situ identification of microorganisms.

L9 ANSWER 6 OF 10 SCISEARCH COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER: 2000:604507 SCISEARCH
THE GENUINE ARTICLE: 340QP
TITLE: Unlabeled **helper oligonucleotides** increase the in situ accessibility to 16S rRNA of fluorescently labeled **oligonucleotide** probes
AUTHOR: Fuchs B M (Reprint); Glockner F O; Wulf J; Amann R

CORPORATE SOURCE: MAX PLANCK INST MARINE MIKROBIOL, CELSIUSSTR 1, D-28359 BREMEN, GERMANY (Reprint)
COUNTRY OF AUTHOR: GERMANY
SOURCE: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (AUG 2000) Vol. 66, No. 8, pp. 3603-3607.
Publisher: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904.
ISSN: 0099-2240.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; AGRI
LANGUAGE: English
REFERENCE COUNT: 17

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB **Target** site inaccessibility represents a significant problem for fluorescence in situ **hybridization** (FISH) of 16S rRNA with **oligonucleotide** probes. Here, unlabeled **oligonucleotides** (helpers) that bind adjacent to the **probe target** site were evaluated for their potential to increase weak **probe hybridization** signals in Escherichia coli DSM 30083(T). The use of helpers **enhanced** the fluorescence signal of all six probes examined at least fourfold. In one case, the signal of **probe** Eco474 was increased 25-fold with the use of a single **helper probe**, H440-2. In another case, four unlabeled helpers raised the FISH signal of a formerly weak **probe**, Eco585, to the level of the brightest monolabeled **oligonucleotide** probes available for E. coli, The temperature of dissociation and the mismatch discrimination of probes were not significantly influenced by the addition of helpers. Therefore, using helpers should not cause labeling of additional nontarget organisms at a defined stringency of **hybridization**, However, the **helper** action is based on sequence-specific binding, and there is thus a potential for narrowing the **target** group which must be considered when designing helpers, We conclude that helpers can open inaccessible rRNA regions for FISH with **oligonucleotide** probes and will thereby further improve the applicability of this technique for in situ identification of microorganisms.

L9 ANSWER 7 OF 10 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:812019 CAPLUS
DOCUMENT NUMBER: 137:333989
TITLE: LNA **helper** probes for detection of a single nucleotide polymorphism by a capture **oligonucleotide**
INVENTOR(S): Jacobsen, Nana; Jakobsen, Mogens Havsteen; Skouv, Jan
PATENT ASSIGNEE(S): Exiqon A/S, Den.
SOURCE: Eur. Pat. Appl., 24 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1251183	A2	20021023	EP 2002-388014	20020218

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRIORITY APPLN. INFO.: US 2001-284729P P 20010418

AB The invention relates to a method for **enhancing hybridization** of a capture **oligonucleotide** to a **target** sequence using a **helper probe**

comprising modified nucleotide residues. The said capture oligonucleotide or amplicon is conjugated to a reporter group. The method exhibits significantly improved binding abilities of capture oligonucleotide to target sequence. In particular the method is suitable for detection of single nucleotide polymorphism or genotyping a human or animal.

L9 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:51666 CAPLUS
DOCUMENT NUMBER: 136:97271
TITLE: Dipstick assays for detection and capture of target nucleic acids in solution using helper probes
INVENTOR(S): Lee, Helen; Dineva, Magda Anastassova; Hazelwood, Shaun Christopher
PATENT ASSIGNEE(S): UK
SOURCE: PCT Int. Appl., 69 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002004668	A2	20020117	WO 2001-GB3024	20010706
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 2001067752	A5	20020121	AU 2001-67752	20010706
PRIORITY APPLN. INFO.:			GB 2000-16814 A	20000707
			WO 2001-GB3024 W	20010706

AB Use of helper probes in dipstick assays is described. A dipstick assay is used to test for the presence of a target nucleic acid in a sample soln. The sample soln. is contacted with the dipstick contact end to cause the sample soln. to move by capillary action to a capture zone of the dipstick where the target nucleic acid is captured by a capture probe.. A labeled detection **probe** is provided that **hybridizes** to one region of the **target** nucleic acid and contains a detection ligand, while the capture **probe** which **hybridizes** to another region of the **target** nucleic acid contains a capture ligand. Helper probes may be used to **enhance** the binding of the capture and/or detection probe to the target nucleic acid, thereby improving the sensitivity of target nucleic acid detection. The first helper probe binds to a second sequence of the target nucleic acid which is either adjacent to the first sequence or is spaced up to 10 nucleotides from the first sequence. The second helper probe binds to a third sequence of the target nucleic acid which is either 10 nucleotides away from or adjacent to the first sequence. Hence, the second and third sequences flank the first sequence of the target nucleic acid. The detection **probe** may comprise a hook detection **probe** which **hybridizes** to a fourth sequence of the **target** nucleic acid and a universal detection **probe** which

hybridizes to the hook detection **probe**. Also, a third helper probe which binds to a fifth sequence of a target nucleic acid may be included to **enhance** binding of the detection probe to the fourth sequence of the target nucleic acid. The capture probe may comprise a universal capture probe **hybridized** to a hook capture probe. A complex may be formed between the detection probe, the first helper probe and the target nucleic acid in soln. which moves up to the capture zone by capillary action where the capture probe contacts the target nucleic acid. Alternatively, a quaternary complex may be formed between the target nucleic acid, detection probe, capture probe and helper probe in soln. prior to binding a capture moiety at the capture zone of the dipstick. In other methods, the helper probes, detection probes or capture probe may also be immobilized to the region between the contact and capture zones and released upon binding the target nucleic acid or they may be releasably immobilized at the capture zone. Dipsticks and kits are also described for diagnosis of sexually transmitted diseases like Chlamydia.

L9 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:552840 CAPLUS
DOCUMENT NUMBER: 134:37611
TITLE: Unlabeled **helper oligonucleotides** increase the in situ accessibility to 16S rRNA of fluorescently labeled **oligonucleotide** probes
AUTHOR(S): Fuchs, Bernhard M.; Glockner, Frank Oliver; Wulf, Jorg; Amann, Rudolf
CORPORATE SOURCE: Max-Planck-Institut fur Marine Mikrobiologie, Bremen, D-28359, Germany
SOURCE: Applied and Environmental Microbiology (2000), 66(8), 3603-3607
CODEN: AEMIDF; ISSN: 0099-2240
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Target site inaccessibility represents a significant problem for fluorescence in situ **hybridization** (FISH) of 16S rRNA with oligonucleotide probes. Here, unlabeled oligonucleotides (helpers) that bind adjacent to the **probe target** site were evaluated for their potential to increase weak **probe hybridization** signals in Escherichia coli DSM 30083T. The use of helpers **enhanced** the fluorescence signal of all six probes examd. at least fourfold. In one case, the signal of probe Eco474 was increased 25-fold with the use of a single helper probe, H440-2. In another case, four unlabeled helpers raised the FISH signal of a formerly weak probe, Eco585, to the level of the brightest monolabeled oligonucleotide probes available for E. coli. The temp. of dissocn. and the mismatch discrimination of probes were not significantly influenced by the addn. of helpers. Therefore, using helpers should not cause labeling of addnl. nontarget organisms at a defined stringency of **hybridization**. However, the helper action is based on sequence-specific binding, and there is thus a potential for narrowing the target group which must be considered when designing helpers. We conclude that helpers can open inaccessible rRNA regions for FISH with oligonucleotide probes and will thereby further improve the applicability of this technique for in situ identification of microorganisms.
REFERENCE COUNT: 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE
FORMAT

L9 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1990:154800 CAPLUS
DOCUMENT NUMBER: 112:154800
TITLE: **Helper oligonucleotides** for **enhancing** nucleic acid **hybridization** assays, their use, and a kit containing them
INVENTOR(S): Hogan, James John; Milliman, Curt Lawrence
PATENT ASSIGNEE(S): ML Technology Ventures, L. P., USA
SOURCE: Eur. Pat. Appl., 17 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 318245	A2	19890531	EP 1988-311036	19881122
EP 318245	A3	19900912		
EP 318245	B1	19940608		
R: AT, BE, CH, DE, ES, FR, GB, GR, IT, LI, LU, NL, SE				
US 5030557	A	19910709	US 1987-124975	19871124
AT 106947	E	19940615	AT 1988-311036	19881122
ES 2056115	T3	19941001	ES 1988-311036	19881122
WO 8904876	A1	19890601	WO 1988-US4103	19881123
W: AU, DK, FI, JP, KR, NO				
AU 8826112	A1	19890614	AU 1988-26112	19881123
AU 613989	B2	19910815		
JP 02502250	T2	19900726	JP 1989-500216	19881123
CA 1319336	A1	19930622	CA 1988-583849	19881123
FI 8903526	A	19890721	FI 1989-3526	19890721
NO 8902990	A	19890913	NO 1989-2990	19890721
DK 8903612	A	19890920	DK 1989-3612	19890721

PRIORITY APPLN. INFO.:

US 1987-124975		19871124
EP 1988-311036		19881122
WO 1988-US4103		19881123

GI

5'-CCTCCCCGCTGAAAGTACTTTAC-3' I

5'-GGTGCTTCTTCTGCGGGTAACGTCAATGAG-3' II

AB A process is provided for **enhancing** the binding between a nucleotide **probe** and a complementary nucleotide sequence in a single-stranded **target** nucleic acid; the process comprises adding a **helper oligonucleotide** which **hybridizes** with the **target** nucleic acid in a different region than the **probe**, the **helper oligonucleotide** being added in an amt. effective to **enhance** binding of **probe** and **target** nucleic acid. The **helper oligonucleotide** imposes a different secondary and tertiary structure on the target; the resulting hybrid of probe and **helper**-target hybrid also exhibits a higher melting temp. (Tm) than the hybrid which results from the addn. of the probe alone. Thus, assays for Salmonella enteritidis rRNA were performed using